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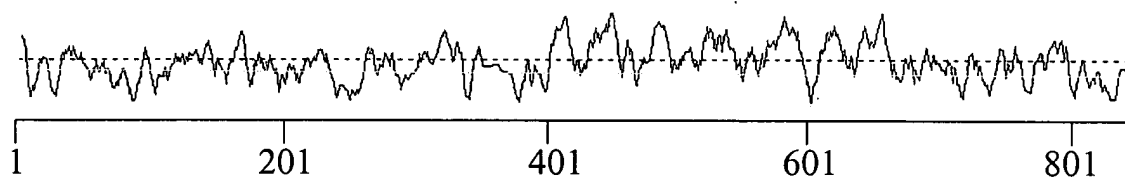


Figure 1

ion_trans: domain 1 of 1, from 472 to 661: score 0.1, E = 1.2
 (SEQ ID NO:9) *->ilfildllfvllflleivlkfiayglkstsniaakylksifnildll
 ++ i + ++f++ ++l +++ ++ y ++ +
 52906 472 DWRIAMTYERIFFICLEILVCAIHPI-----PGNYTFTWTA-RLAF 511
 ailplllllvflfsgteqvakkrlrerfslelsqwyryilrflrlLrllR
 ++ p+ + + + l++ +Lrl+
 52906 512 SYAPS--TTTADV DII-----LSIPMFLRLYL 536
 lLrllrllrrletlf.e.....fe.lgtlaWslqslgralksilrfl111
 + r++ ++ +lf+ ++++++ l ++ +k+++ ++ +
 52906 537 ---IARVMLLHSKLFtDtssrsIGaLNKI---NFNTRFVMKTLMTICPGT 580
 lllligfsvigyllfkgyedlsenevdgnsefssyfdafyflfvtl1ttvG
 +ll++ s+ ++++ + + +e+ d+ + s++ a++ +t++++G
 52906 581 VLLVF--SISLWIIAAWTVRACERYHDQQDVTSNFLGAMWLISITFLSIG 628
 fGdlvpvwlgiiffvlf ffiivgl111lnlliavi<-*
 +Gd+vp++++ ++l+ i+g ++l +av+
 52906 629 YGDMVPNTYCGKGVCLLTGIMGAGCTALVVAVV 661

Figure 2

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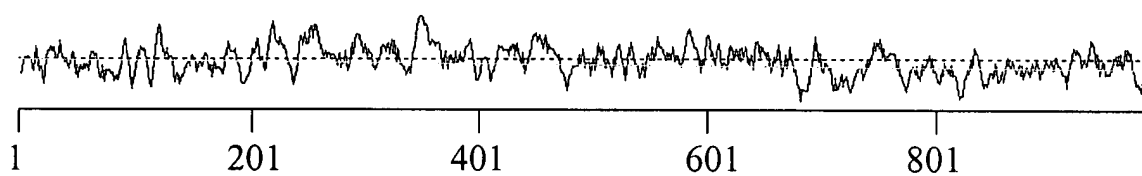


Figure 3

ion_trans: domain 1 of 1, from 247 to 467: score 94.8, E = 1.7e-24
 (SEQ ID NO:9) *->ilfildllfvllfilleivlkfiayglkstsn.....iaak
 +l ld + +++fl++ivl+f+ + + +++++ +++++ i++
 33408 247 WLW-LDSVVDVIFLVDIVLNFH-TT----FVgpggevisdpklIRMN 287
 ylkisifnildllailpllllllvflsgteqvakkrlrerfslelsqwyyr
 ylk++f +dll++lp++++ ++ +++ +
 33408 288 YLKTWfV-IDLLSCLPYDIINAFENVDE-----G 315
 ilrflrlLrllRlLrllrllrrletlfefelgtlaWslqslg.ralksil
 i +++++L+ +R llrl r+ ++ l + l +++ ++
 33408 316 ISSLFSSLKVVR---LLRLGRVARK-----LDHY---LEYGAaVLVLLVC 354
 rfllllllllligfsvigyllfkgyedlse.....
 f+l++++l +++++ ig + + ++ + +++ + +++ ++
 33408 355 VFGLVAHWLACIWYSIGDYEVIDEVTNTIqidswlyqlalsigtpyrynt 404
 ...nevdgnsefssyfdafyflfvltttvGfGdlvpv.wlgiiffvlffi
 + + +++g+s+ s y ++yf++++l++GfG++ p++ +++f v++++
 33408 405 sagIWEggPSKDSLYVSSLYFTMTSLTTIGFGNIAPTtDVEKMFSVAMMM 454
 ivgllllnllliavi<-*
 +++ ll ++++++
 33408 455 VGS-LLYATIFGNV 467

Figure 4A

cNMP_binding: domain 1 of 1, from 565 to 655: score 78.3, E = 1.5e-19
 (SEQ ID NO:10) *->aleersypaGeviirGdpgdsfYivlsGeveykltdGartpevs
 ++ + ++G+ i++ G+ d + +v+sG++ev++
 33408 565 EFQTIHCAPGDLIYHAGESVDALCFVVGSLVLIQ----- 599
 qkqdtreqvvatlpgGdfFGElaalltndgnknnavlpsldqgaprtatvra
 +++vva+lg+Gd+FG++ + + + +a+ a+vra
 33408 600 -----DDEVVAILGKGdVFGDIFW-KE-----TTLAHACANVRA 632
 ltdsellrldredFrrllqkype<-*
 lt+++l+ + re+++ +l+ y +
 33408 633 LTYCDLHIIKREALLKVLDFYTA 655

Figure 4B

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33408
rat EAG2
(SEQ ID NO:12)

MPGGKRGGLVA PQNTFLENIV RRSSESSFLL GNAQIVDWPV VYSNDGFCKL
MPGGKRGGLVA PQNTFLENIV RRSSESSFLL GNAQIVDWPV VYSNDGFCKL

SGYHRADVMQ KSSTCSFMYG ELTDKKTIEK VRQTFDNYES NCFEVLLYKK
SGYHRADVMQ KSSTCSFMYG ELTDKKTIEK VRQTFDNYES NCFEVLLYKK

NRTPVWFYMQ IAPIRNEHEK VVLFLCTFKD ITLTKQPIED DSTKGWTKFA
NRTPVWFYMQ IAPIRNEHEK VVLFLCTFKD ITLTKQPIED DSTKGWTKFA

RLTRALTNSR SVLQQLTPMN KTEVVHKHSR LAEVLQLGSD ILPQYKQEAP
RLTRALTNSR SVLQQLTPMN KTETVHKHSR LAEVLQLGSD ILPQYKQEAP

KTPPHIILHY CAFKTTWDWV ILILTFYTAI MVPYNVSFKT KQNNIAWLVL
KTPPHIILHY CAFKTTWDWV ILILTFYTAI MVPYNVSFKT KQNNIAWLVL

DSVVDVIFLV DIVLNFHTTF VGPGEVISED PKLIRMNYLK TWFVIDLLSC
DSVVDVIFLV DIVLNFHTTF VGPGEVISED PKLIRMNYLK TWFVIDLLSC

LPYDIINAFE NVDEGISSLF SSLKVVRLLR LGRVARKLDH YLEYGA AVL
LPYDIINAFE NVDEGISSLF SSLKVVRLLR LGRVARKLDH YLEYGA AVL

LLVCVFGLVA HWLACIWYSI GDYEVIDEVT NTIQIDSWLY QLALSIGTPY
LLVCVFGLVA HWLACIWYSI GDYEVIDEVT NTIQIDSWLY QLALSIRTPY

RYNTSAGIWE GGPSKDSLYV SSlyFTMTSL TTIGFGNIAP TTDVEKMFSV
RYNTSAGIWE GGPSKDSLYV SSlyFTMTSL TTIGFGNIAP TTDVEKMFSV

AMMMVGSLLY ATIFGNVTTI FQQMYANTNR YHEMLNNVRD FLKLYQVPKG
AMMMVGSLLY ATIFGNVTTI FQQMYANTNR YHEMLNNVRD FLKLYQVPKG

LSERVMDYIV STWSMSKGID TEKVLSICPK DMRADICVHL NRKVFNEHPA
LSERVMDYIV STWSMSKGID TEKVLSICPK DMRADICVHL NRKVFNEHPA

FRLASDGCLR ALAVEFQTIH CAPGDLIYHA GESVDALCFV VSGSLEVIQD
FRLASDGCLR ALAVEFQTIH CAPGDLIYHA GESVDALCFV VSGSLEVIQD

DEVVAILGKG DVFGDIFWKE TTLAHACANV RALTYCDLHI IKREALLKVL
EEVVAILGKG DVFGDIFWKE TTLAHACANV RALTYCDLHI IKREALLKVL

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Figure 4C

DFYTAFANSF SRNLT LTCNL RKRIIFRKIS DVKKEEEERL RQKNEVTLSI
DFYTAFANSF SRNLT LTCNL RKRIIFRKIS DVKKEEEERL RQKNEVTLSI

PVDHPVRKLF QKFKQQKELR NQGSTQGDPE RNQLQVESRS LQNGTSITGT
PVDHPVRKLF QKFKQQKELR NQGSAQSDPE RSQLQVESRP LQNGASITGT

SVVTVSQITP IQTSLAYVKT SESLKQNNRD AMELKPNGGA DQKCLKVNSP
SVVTVSQITP IQTSLAYVKT SETLKQNNRD AMELKPNGGA EPKCLKVNSP

IRMKNGNGKG WLRLKNNMGA HEEKKEDWNN VTKAESMGLL SEDPKSSDSE
IRMKNGNGKG WLRLKNNMGA HEEKKEEWN VTKAESMGLL SEDPKGSDSE

NSVTKNPLRK TDSCDSGITK SDLRLDKAGE ARSPLEHSPI QADAKHPFYP
NSVTKNPLRK TDSCDSGITK SDLRLDKAGE ARSPLEHSPS QADAKHPFYP

IPEQALQTTL QEVKHELKED IQLLS CRMTA LEKQVAEILK ILSEKSV PQA
IPEQALQTTL QEVKHELKED IQLLS CRMTA LEKQVAEILK LLSEKSV PQT

SSPKSQMPLQ VPPQIPCQDI FSVSRPESPE SDKDEIHF
SSPKPQIPLQ VPPQIPCQDI FSVSRPESPE SDKDEINF

Figure 4D

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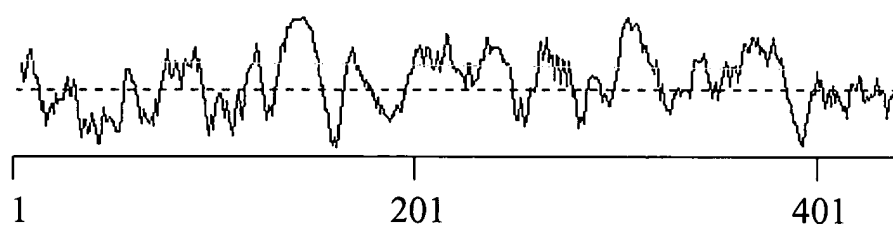


Figure 5

K_tetra: domain 1 of 1, from 3 to 101: score 169.0, E = 7.9e-47
 (SEQ ID NO:11) *->ErvrLNVGGkrFeTskstLtrfkpdTlLgrllktdsdvhearlrld
 Er++LNV G+rFeT+++TL rf pdTlLg++++ r ++
 12189 3 ERLVLNVAGLRFETRARTLGRF-PDTLLGDPAR-----R-GR 37

fyddetgEyFFDRsPkhFetILnfYRtGdGkLhrp.evcldsfleEleFy
 fydd++ EyFFDR++++F+++L++Y++G G+L+rp +v+ld+fleE +Fy
 12189 38 FYDDARREYFFDRHRPSFDAVLYYYQSG-GRLRRPaHVPLDVFL EEVAFY 86

gldelaiesCcedey<-*
 gl+ a++ +ede+
 12189 87 GLGAAALARLREDEG 101

Figure 6A

ion_trans: domain 1 of 1, from 198 to 383: score 144.8, E = 1.5e-39
 (SEQ ID NO:9) *->ilfildllfvllfllleivlkfiayglkstsniaakylksifnildll
 ++f++++l++ +f +e++++ ++ k a ++k+++n++d+
 12189 198 PFFVVETLCICWFSELLVRLVCPSK-----AIFFKNVMNLIDFV 238

ailpllllllvflsgteqvakkrlrerfslelsqwyrrilrflrlLrllR
 ailp+++ l+ l+++ +++++ + +L +lR
 12189 239 AILPYFVALGTELARQ-----RGVGQQAMSLAILR 268

lLrllrllrrletlfefelgtlawslqslg.ralksilrfllllllllig
 ++rl+r++r ++ + +++ lq+lg+++ +s+ ++l++l+ig
 12189 269 VIRLVRVFRIFKLSR---HSKG---LQILGqTLRASMRELGLLIFFLFIG 312

fsvigyllfkgyedlsenevdgnsefssyfdafyflfvltlttvGfGdlvp
 + +++ +++++ + d+ +s f+s++++f++++vt+ttvG+Gd+ p
 12189 313 VVLFSSAVYFAEVDVRV-----DSHFTSIPESFWWAVVTMTTVGYGDMAP 356

v.wlgiiffvlfiiivgllllnllliavi<-*
 v+++g+i++ ++++i+g+l+++l+++vi
 12189 357 VtVGGKIVG-SLCAIAGVLTISLPVPVI 383

Figure 6B

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 T09090-T0957860

Mouse Kv1.7
(SEQ ID NO:13)
12189

MTTRKAQEIH GKAPGGSVST GVGTAEGAPS PAGVTPPPPP RPGRTFHAIF
.....

TRRHRTPDWG GCGVGATRPF TGRPGCARHG ATVPAALRCC ERLVLNVAGL
.....CC ERLVLNVAGL

RFETRARTLG RFPDTLLGDP VRRSRFYDGA RAEYFFDRHR PSFDAVLYYY
RFETRARTLG RFPDTLLGDP ARRGRFYDDA RREYFFDRHR PSFDAVLYYY

QSGGRLRRPA HVPLDVFLEE VSFYGLG.RR LARLREDEGC AVA.ERPLPP
QSGGRLRRPA HVPLDVFLEE VAFYGLGAAA LARLREDEGC PVPPERPLPR

.PFARQLWLL FEFPESSQAA RVLAVVSVLV ILVSIVVFCL ETLPDFRDDR
RAFARQLCLL FEFPESSQAA RVLAVVSVLV ILVSIVVFCL ETLPDFRDDR

DDPGLAPVAA ATGSFLARLN GSSPMGPAPP RQPFNDPFFV VETLCICWFS
DGTGLA.AAA AAGPFPAPLN GSSQMPGNPP RLPFNDPFFV VETLCICWFS

FELLVHLVAC PSKAVFFKNV MNLIDFVAIL PYFVALGTEL ARQRGVGQPA
FELLVRLLVC PSKAIFFKNV MNLIDFVAIL PYFVALGTEL ARQRGVGQQA

MSLAILRVIR LVRVFRIFKL SRHSKGLQIL GQTLRASMRE LGLLIFFLFI
MSLAILRVIR LVRVFRIFKL SRHSKGLQIL GQTLRASMRE LGLLIFFLFI

GVVLFSSAVY FAEVDRVDTH FTSIPESFWW AVVTMTTVGY GDMAPVTVGG
GVVLFSSAVY FAEVDRVDSH FTSIPESFWW AVVTMTTVGY GDMAPVTVGG

KIVGSLCAIA GVLTISLPVP VIVSNFSYFY HRETEGEEAG MYSHVDTQPC
KIVGSLCAIA GVLTISLPVP VIVSNFSYFY HRETEGEEAG MFSHVDMQPC

GTLEGKANGG LVDSEVPELL PPLWPPAGKH MVTEV
GPLEGKANGG LVDGEVPELP PPLWAPPGKH LVTEV

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Figure 6C